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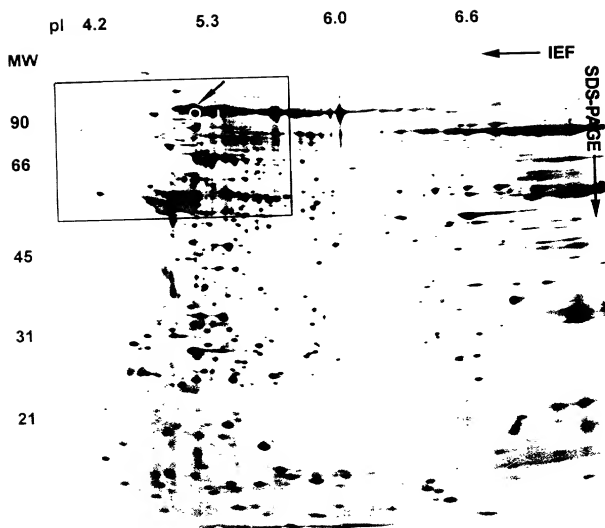


FIG. 1A



FIG. 1B

FIG. 1C

FIG. 1D

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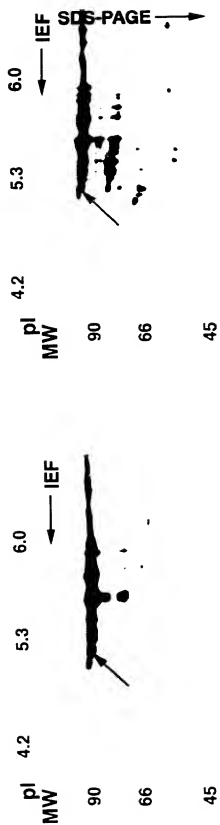


FIG. 2A

FIG. 2B

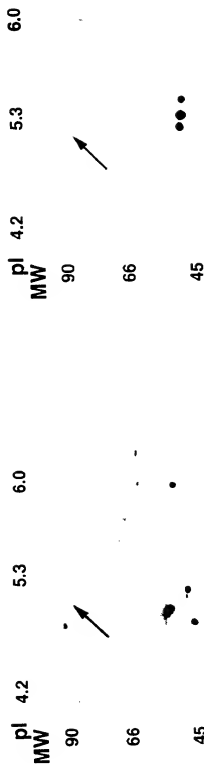


FIG. 2C

FIG. 2D

FIG.3A

1141 AAAGAGGTGGTCTCGGATCTCATGCGATCCTTCTTGAGGAATCTCCACAGCGTCACAGGG  
 K E V V S D L I D S F L R N L H S V T G 346  
 1201 ACCCTCATGACTGACACACAGTTTGTCTCGGCTGTGAAAAGAAGTGTCTTCTCATGGA  
 T L M T D T Q F V S A V K R T V F S H G 366  
 1261 AGCCAAAAGGCCACAGATATCATGGATGCCATGCTAAGGAAGCTGTACAATGTAATGTTT  
S Q K A T D I M D A M L R K L Y N V M F 386  
 1321 GCCAAGAAAGTCCCTGAGCATGTCAGGAAGCCCAAGACAAGGCTGTGAGTATTCCCTC  
 A K K V P E H V R K A Q D K A V S Y S L 406  
 1381 ATCTCCATGAAAGGAATGGGTGATCCTAAAAACCGAAATGTGAACCTTTGCCATGAAATCT  
I S M K G M G D P K N R N V N F A M K S 426  
 1441 GAACTAAATTGAGAGAAAAATGTATTCTGAACCCAAATCAGAGGAGAGACTTGTGGC  
 E T K L R E K M Y S E P K S E E E T C A 446  
 1501 AAAACTCTGGGTGAGCACATTATCAAAGAGGGGCTTACCCTGTGGCATAAAAGTCAGCAG  
 K T L G E H I I K E G L T L W H K S Q Q 466  
 1561 AACGAATGTAATCTCTAGGTTTCCAGCATGCAGCATTGGAAGCTCCCAACACACAGCGT  
 N E C K S L G F Q H A A F E A P N T Q R 486  
 1621 AAGCGCTCATCAGACATTTCCCTTGAAGTACCCCTGAAGATACTGGCAACCTCAGCCTTCCT  
 K P A S D I S F E Y P E D T G N L S L P 506  
 1681 CCATATCCTCCAGAGAAACCTGAGAATTTTATGTATGATTGAGTCTCTGGGCCAAGGAC  
 P Y P P E K P E N F M Y D S D S W A K D 526  
 1741 CTGATCGTGTCTGCCCTGCTTCTGATTCAATATCACCTGGCCCAGGGAGGAAGAAGGGAT  
 L I V S A L L L L I Q Y H L A Q G G R R D 546  
 1801 GCACGGAGCTTCGTTGAAGCTGCTGGCACCACCAACTTTCCTGCCAATGAACCTCCTGTA  
 A R S F V E A A G T T N F P A N E P P V 566  
 1861 GCTCCCGATGAATCTTGCCCTTAAGTCTGCTCCCATTTGAGTGACCAAGAACAAGCAGAA  
 A P D E S C L K S A P I V G D Q E Q A E 586  
 1921 AAGAAGGACCTAAGGAGTGTTTTCTTTAATTCATCCGAACCTTACTTAGTGAGACCAT  
 K K D L R S V F F N S I R N L L S E T I 606  
 1981 TTCAAGCGTGACCAGAGCCCTGAACCCAAGTGCCGGAACAGCCAGTTAAGGAAGATAGG  
F K R D Q S P E P K V P E Q P V K E D R  
 2041 AAGTTGTGTGAAAGACCGCTTGGCGTCTTCTCCCCCAGGCTATATGAGATGATGAGACC  
 K L C E R P L A S S P P P R L Y E D D E T 646  
 2101 CCTGGTGCCTTTCTGGGCTGACCAAGATGGCTGTGACGCAGATAGATGCCACATGAGT  
P G A L S G L T K M A V S Q I D G H M S 666  
 2161 GGCAGATGGTAGAACCTGTGAACTCAGTCAGTGAAGCTGTGTGTCTCATCTAGTGAAG  
 G Q M V E H L M N S V M K L C V I I A K 686

FIG.3B

2221 TCCTGTGATGCTTCGTTGCCAGACCTGGGAGATGACAAGCTGGGAGATGCCAGTAGGCTA  
       S C D A S L A E L G D D K L G D A S R L 706  
 2281 ACTTCGGCCTTCCCAGATAGTTTATATGAGTGCTTACCAGCCAAGGGCACAGGGTCAGCA  
       T S A F P D S L Y E C L P A K G T G S A 726  
 2341 GAAGCTGTCCTGCAGAATGCCTATCAAGCTATCCATAACGAAATGAGAGGCACATCAGGA  
       E A V L Q N A Y Q A I H N E M R G T S G 746  
 2401 CAGCCCCCTGAAGGGTGTGCAGCACCCACGGTGATTGTCAGCAATCACAACCTAACGGAC  
       Q P P E G C A A P T V I V S N H N L T D 766  
 2461 ACAGTTCAGACAAGCAACTCCAAGCCGTCCTTCAATGGGTAGCTGCCTCTGAGCTCAAT  
       T V Q N K Q L Q A V L Q W V A A S E L N 786  
 2521 GTCCTATTTTGATTTTCTGGTGATGATGAAGGGATCCAGGAGAAGCTACTTCAGCTC  
       V P I L Y F A G D D E G I Q E K L L Q L 806  
 2581 TCAGCTGCTGCTGTGGACAAAGGATGCAGTGTGGGCGAGGTTCTGCAGTCGGTGCTGCGC  
       S A A A V D K G C S V G E V L Q S V L R 826  
 2641 TATGAGAAGGAGCGCCAGCTGAATGAGGCGGTGGGGAATGTCACACCGCTGCAGCTGCTG  
       Y E K E R Q L N E A V G N V T P L Q L L 846  
 2701 GACTGGCTGATGGTGAACCTGTAATCGGCAACCCACTGCTTTCCCTCTTCTGGCAGTG  
       D W L M V N L \* 853  
 2761 GGGCGCGCCCTTATCCCGCCCTTCTTTCTCACTTCCACATCTCCCCCTCTATATCCTCA  
 2821 CAGAGCCCTAACATTATCTTCACACCACCTCTCATCAAAGACATGTCATCTTGTGCTAGCC  
 2881 ACTGGATTTGCAGATTTTCTGTCCGTGCAAGCAAGGACGTAATAATAAAAATTACAA  
 2941 TG

FIG.3C

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1            10            20            30            40            50  
 FSP95 MSEKVDWLQSQNGVCKVDVYSPGDNAQDW...MTTSDPVRVLSWLRDLEKSTAE  
 mouse MSDDIWLHHSRRGVCKVDLYSPKGGQDQDKVLCFVDVSTLNMEDKDSKGAAGSRSEGE  
 human MSDDIWLHRSRGVCKVDLYNPFEGQDQDKVLCFVDVSTLNMEDKDYKDAASSSEGN  
 60            70            80            90            100            110  
 FSP95 FQDVRFKPGESFGGETSNSGDPHKGFSDVYNTTTKGTPERLHEFMTHKELPQGPRA  
 mouse LNLLELEEKIIIVIKDTEKQDSKTEGVSCLFKQAPSDPISVLNLLNDLQKYLQGFQH  
 human LNLGSLLEEKIIIVIKDTEKKQDSKTEGVSCLFKQAPSDPVSVLNLSDLQKYLQGFQH  
 120            130            140            150            160            170  
 FSP95 QLCNGSSV.....DEVSFYANRLTNLMIAMARKEITN...EKIDGSENKCVYQSLYMGNE  
 mouse ALSPSASSCKHKVGDLGEGYSKIPSENCYSVYADQVNFVDYLNKGPQNLRLLEMAASKNTN  
 human ELSPSTSTCKHKVGDLTEGDIHRASSENCYSVYADQVNIIDYLMNRPQNLRLLEMTAAKNTN  
 180            190            200            210            220            230  
 FSP95 PPTPKLSKIASLVN...ETVSACSRNAPDKAPGSGDRVSGSSQSPPNLYKISTLK....  
 mouse NNQSPSPNATKSPSNORSVATPEGECSMDLSFYVNRSLSLVIQMARKEIKDKLEGGSK  
 human NNQSPSAPPAPKPPSTORAVISPDGECSDLSFYVNRSLSLVIQMAHKEIKDKLEGGSK  
 240            250            260            270            280            290  
 FSP95 .....IKESTKERRGPDQPPSKKSFYKEVFE.....SRNGDYAREGGR...FFPR  
 mouse CLHHSMYTS.GDKKTSPPSAVSKIASEMAEAVELTSSMRNGCEDQDQGRKTFILYS  
 human CLHHSICPSPGNKERISRTPAKSIASEMAEAVELTAAEMRGITGEFSREGGQKSELYS  
 300            310            320            330            340            350  
 FSP95 E.....RRFRGQERPDFTASVGEITMIYANVSDMMVSTIMTKLTQVQKDTITL  
 mouse EMCNKNKCKEKQOMCPKDSKEFADSIKGLMYYANVASDMMVSMVKTLKVHSCGKPIIP  
 human ELSNKSCKSGDKIQMSQRESKFEADSIKGLMYYANVASDMMVSLMVKTLKVHSSGKPIIP  
 360            370            380            390            400            410  
 FSP95 ATITLLKVVLLKHAKVVSVDLIDSLRNLSVGTGLMTDITQFSVAVKRTVFSHGSKATD  
 mouse ACVVLLKRVLLKHAKVVSVDLIDSLRNLSVGTGLMTDITQFSVAVKRNLFNHGKQNAAD  
 human ASVVLLKRVLLRHAKVVSVDLIDSLRNLSVGTGLMTDITQFSVAVKRNLFNWKQNAAD  
 420            430            440            450            460            470  
 FSP95 ITMDAMLRKLYNMFAKKVPEHVRKAQDKAVYSLSLSMKQMGDPKRNRYNF...AMKSET  
 mouse ITMEAMLRKLYNSALLOEK.....KETKSQSLAYAPLK.AGTNDPKCKNOSLEFSAMKAE  
 human ITMEAMLRKLYNSALIGEE.....KETKSQSLAYASLK.AGSHDPKCRNOSLEFSAMKAE  
 480            490            500            510            520            530  
 FSP95 KLERK...MYSEPKSEETQAKTLGEHTIKEGLTLWHKSGQNECKSLGFQHAFAEPNT  
 mouse KQDKCKTSKADPCCKSLTSAERVSEHILKESLTMMNTQKQNGCKVTKNVCQTSKDEKR  
 human KERDKCKMKSDPCKSLTSAERVSEHILKESLTWNQKQNGCKVATK.ACSNKDEKG

FIG.4A

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FSP95 540 550 560 570 580 590  
 QKPADISFEYPEDTGNLSPPYPPEKPFNFMYDSSWAKDLIVSALLLIQYHLAAGG  
 mouse EKISPTSDSLAKDLIVSALLLIQYHLTQQA...AKDPCEEECPGSSM...GYMSQSA  
 human EKINASTDSLAKDLIVSALLLIQYHLTQQT...GKDTCEEDCPGSTM...GYMAQST  
 600 610 620 630 640  
 FSP95 RRARSFVEAAGTTTFPANPPVAPDESOLKSAPIVGDOEAQEKDLRSVFFNSIRNLL  
 mouse QYEKCGGQSSKSLSMKHFEITRGAPGFSTCMKE...NQ...LESGKMDMSNMVLSLIQKLL  
 human QYEKCGGQSSAKALSVKQLSHRAPGPSTCQKE...NQHLDSQKMDMSNIVLMLIQKLL  
 650 660 670 680 690 700  
 FSP95 SETIFKROQSPPEPKVPEQPVKEIDFKLCERPLASSPRLYEDETPGALSGLTKMAVSQI  
 mouse SESPFSCDELTE...SDNKRCDPRSSKAAPMAKR...PEEQCQDNAELDFISG  
 human NENPEKCDPCE...GENK...CSEPRASKAASMSNRSDKAEQCCQEHQELDCTSG  
 710 720 730 740 750 760  
 FSP95 DGHMSSOMVEHLMNSVMKLCVITAKSCDASLAEIGDDKLGDA SRLTSAFPDSL YECLPA  
 mouse MKQMNROFIDQLVESVMKLCILMAKYRNNGAA...LGELEE...  
 human MKQANGQFIDQLVESVMKLCILMAKYSNDGAA...LAELEE...  
 770 780 790 800 810 820  
 FSP95 KGTGSAAVLQNAAYCAIHNEMRGTSGOPPEGCAAPTIVISNHNLTDTVQNKQLQAVLQW  
 mouse ...QAALVGS...GSRGGRDAMMSQNYSETPGPEVIVNNQCSITINLQ...KQLQAVLQW  
 human ...QAASANKPNFRGTRCIHSGAMPQNYQDSLCHVIVNNQCSITINLQ...KQLQAVLQW  
 830 840 850 860 870 880  
 FSP95 VAASELNVPILYFACDDEGIQEKLLQLSAAAMDKGCSVGEVLQSVLRYEKERQLNEAVG  
 mouse IAAQFNVPMLYFMGDDGGQLEKLPVSAKAAEKGYSGVGLLQEVNMFAKERQLDEAVG  
 human IAAQFNVPMLYFMGDDGGQLEKLPVSAKAAEKGYSGVGLLQEVNMFAKERQPDEAVG  
 890 900  
 FSP95 NVTPLQLLDWLLMNL  
 mouse NMARKQLLDWLLANL  
 human KVARKQLLDWLLANL

FIG.4B

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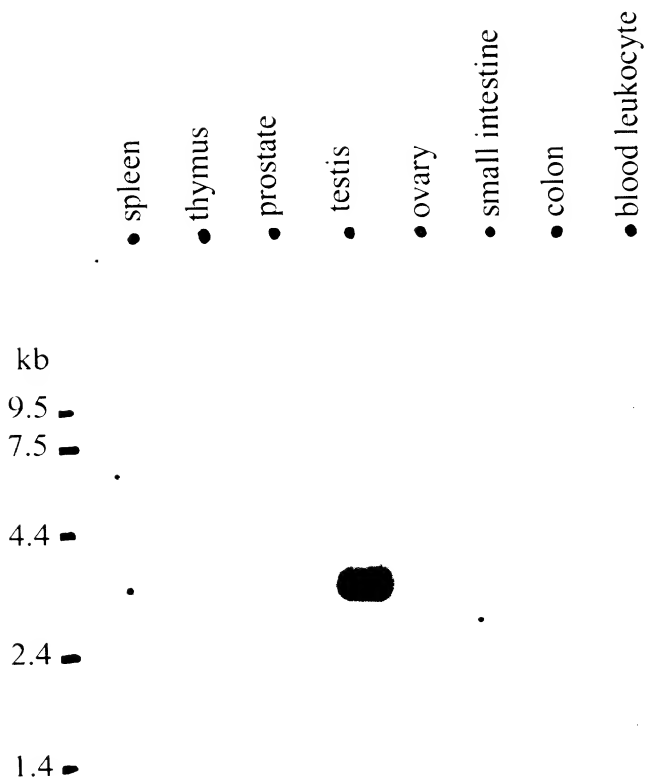


FIG.5A



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|    |    |    |    |    |    |    |    |
|----|----|----|----|----|----|----|----|
| A1 | A2 | A3 | A4 | A5 | A6 | A7 | A8 |
| B1 | B2 | B3 | B4 | B5 | B6 | B7 | B8 |
| C1 | C2 | C3 | C4 | C5 | C6 | C7 | C8 |
| D1 | D2 | D3 | D4 | D5 | D6 | D7 | D8 |
| E1 | E2 | E3 | E4 | E5 | E6 | E7 | E8 |
| F1 | F2 | F3 | F4 | F5 | F6 | F7 | F8 |
| G1 | G2 | G3 | G4 | G5 | G6 | G7 | G8 |

FIG.5B

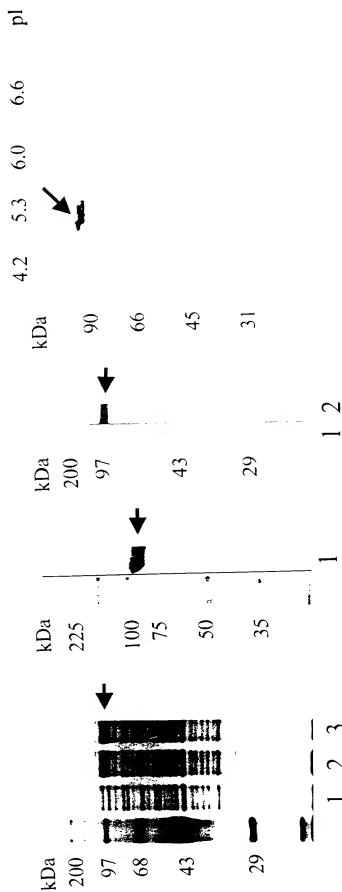


FIG. 6A

FIG. 6B

FIG. 6C

FIG. 6D

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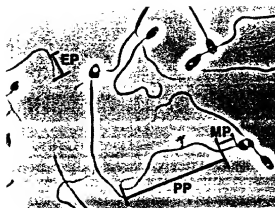


FIG.7A



FIG.7B

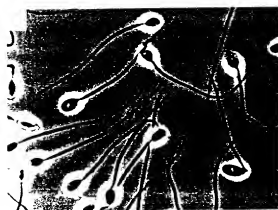


FIG.7C

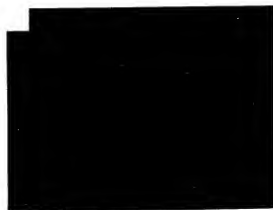


FIG.7D

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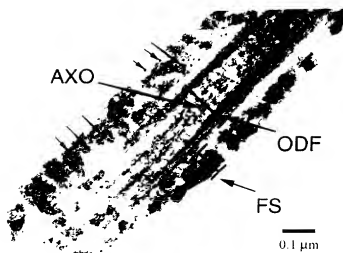


FIG.8A

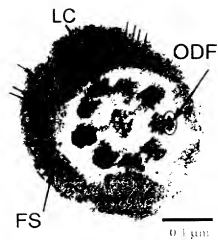


FIG.8B

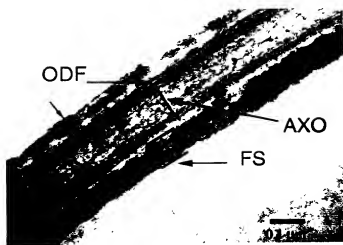


FIG.8C

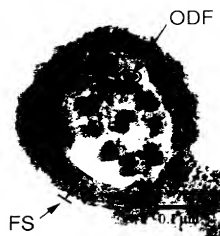


FIG.8D

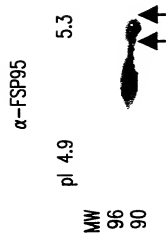


FIG.9A



FIG.9C

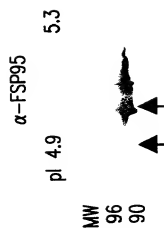
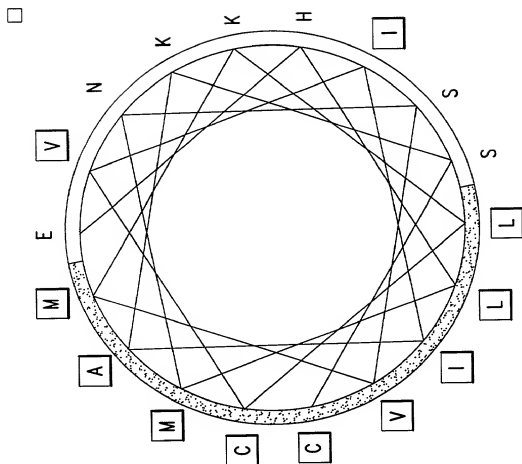


FIG.9B



FIG.9D



RESIDUES: E H L M N S V M K L C V I I A K S C  
 671 688

FIG.10